

Appl. No. : 09/995,938
Filed : November 27, 2001

REMARKS

Claims 1-27 are pending and subject to restriction. Claims 1, 6-8, 13, 14, 17, 22, and 23 have been amended to clarify that they cover the BRZ1 and BZR2 forms of brassinazole resistant (BRZ) proteins and nucleic acid sequences. Support for this amendment can be found at page 5, line 3 of the specification.

It Would Not Impose a Serious Burden to Examine All Claimed Nucleotide Sequences

The Examiner has alleged that the recited nucleotide sequences are structurally distinct chemical compounds and are unrelated to each other. Thus, methods of transforming plants with these sequences are different inventions. Applicants respectfully traverse.

MPEP §803 provides that “if a search and examination of an application can be made without serious burden, the examiner must examine it on the merits, even though it includes claims to distinct or independent inventions” (emphasis added). Applicants respectfully submit that the claimed nucleic acid sequences (e.g., SEQ ID NOs: 1, 2, 3, and 9), and their corresponding amino acid sequences (SEQ ID NOs: 6, 7, 8 and 10) are so structurally related that they can be examined together without imposing a serious burden on the Examiner.

Specifically, SEQ ID NO: 1 is the nucleic acid sequence encoding the wild-type BZR1 polypeptide (SEQ ID NO: 6). SEQ ID NO: 2 is the nucleic acid sequence encoding the mutant bzl1 polypeptide (SEQ ID NO: 7). There is only a single nucleic acid difference between SEQ ID NO: 1 and SEQ ID NO: 2 (cysteine to threonine at position 2147). Thus, the nucleotide sequences of the wild-type BZR1 and mutant bzl1 genes are over 99% identical. Similarly, there is only a single amino acid difference between SEQ ID NO: 6 and SEQ ID NO: 7 (a proline to leucine substitution at position 234). See Sequence Listing and page 6, lines 6-8, of the specification. Accordingly, the amino acid sequences of the wild-type BZR1 and mutant bzl1 proteins are over 99% identical.

Moreover, it is also noted that SEQ ID NOs: 3 and 9, which correspond to the nucleic acid sequences of the wild-type BZR2 and mutant bzl2 genes only differ by a single nucleotide

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(cysteine to threonine at position 2351). Thus, the nucleotide sequences of the wild-type BZR2 and mutant b zr2 genes are over 99% identical. Similarly, the wild-type BZR2 polypeptide (SEQ ID NO: 8) only differs from the mutant b zr2 polypeptide (SEQ ID NO: 10) by a single amino acid (proline to leucine substitution at amino acid position 233). Thus, the amino acid sequences of the wild-type BZR2 and mutant b zr2 proteins are over 99% identical.

In addition, the wild-type BZR1 and wild-type BZR2 proteins are very similar, having 88% identity and 90% similarity with one another. See specification page 6, lines 20-21. Similarly, the mutant b zr1 and mutant b zr2 proteins also share 88% identity and 90% similarity with one another.

Because of the high degree of identity, it would not be an undue burden on the Examiner to search plants transformed with wild-type and mutant forms of the BZR1 genes together. For the same reason, it would not impose a burden on the Examiner to search for plants the wild-type and mutant forms of the BZR2 genes together. Further, due to the 88% identity and 90% similarity of the BZR1 and BZR2 proteins, it would not be a burden to search transforming plants using any of the recited brassinazole resistant (BRZ) genes.

Regardless of which particular nucleic acid sequence or amino acid sequence is elected, the scope of the Examiner's search would not change. For all of the above reasons, Applicants respectfully request withdrawal of the restriction requirement relating to the individual SEQ ID numbers, and examination of all sequences encompassed by the elected claims.

It is also noted that the Commissioner decided *sua sponte* to partially waive the requirements of 37 CFR § 1.141 and permit a reasonable number of nucleotide sequences to be claimed in a single application. See MPEP § 803.04, citing *Examination of Patent Applications Containing Nucleotide Sequences*, 1192 O.G. 68 (November 19, 1996). It has been determined that normally ten sequences constitute a reasonable number for examination purposes. *Id.* Accordingly, in most cases, up to ten independent and distinct nucleotide sequences will be examined in a single application without restriction. *Id.* As the present application is directed to fewer than 10 nucleic acid sequences, this is a reasonable number for the Examiner to search.

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In order to comply with the requirements of 37 CFR §1.143 Applicants elect Group I, corresponding to Claims 1-23, and 25-26, with traverse. Applicants further elect the nucleic acid sequence of SEQ ID NO: 2 and the amino acid sequence SEQ ID NO: 7, with traverse.

Please charge any additional fees, including any fees for additional extension of time, or credit overpayment to Deposit Account No. 11-1410.

Respectfully submitted,

KNOBBE, MARTENS, OLSON & BEAR, LLP

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By: 

Michael L. Fuller
Registration No. 36,516
Attorney of Record
Customer No. 20,995
(619) 235-8550

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